

## CLAIMS:

1. A B Lymphocyte Stimulator (BLyS) binding polypeptide comprising the amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

2. The polypeptide according to Claim 1, wherein Xaa is Pro or Ser.

3. The polypeptide according to Claim 1, wherein said polypeptides comprises the amino acid sequence: X<sub>1</sub>-X<sub>2</sub>-Asp-X<sub>4</sub>-Leu-Thr-X<sub>7</sub>-Leu-X<sub>9</sub>-X<sub>10</sub> (SEQ ID NO:448), wherein

X<sub>1</sub> is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X<sub>2</sub> is Tyr, Phe, Glu, Cys, Asn;

X<sub>4</sub> is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X<sub>7</sub> is Lys, Asn, Gln, Gly, or Arg;

X<sub>9</sub> is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

X<sub>10</sub> is Leu, Phe, Val, Ile, or His.

4. The polypeptide according to Claim 3, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

5. The polypeptide according to Claim 3, wherein said polypeptide comprises the amino acid sequence: Ala-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Asp-X<sub>6</sub>-Leu-Thr-X<sub>9</sub>-Leu-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:447),

wherein

X<sub>2</sub> is any amino acid except Arg;

X<sub>3</sub> is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X<sub>4</sub> is Tyr, Phe, Glu, Cys, Asn;

X<sub>6</sub> is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X<sub>9</sub> is Lys, Asn, Gln, Gly, or Arg;

X<sub>11</sub> is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X<sub>12</sub> is Leu, Phe, Val, Ile, or His;

X<sub>13</sub> is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X<sub>14</sub> is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

6. The polypeptide according to Claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

7. The polypeptide according to Claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 437-444 as depicted in Table 15.

8. The polypeptide according to Claim 1, comprising an amino acid sequence selected from the group consisting of:

Ala-Gly-Lys-Glu-Pro-Cys-Tyr-Phe-Tyr-Trp-Glu-Cys-Ala-Val-Ser-Gly (SEQ ID NO:450);

Ala-Gly-Val-Pro-Phe-Cys-Asp-Leu-Leu-Thr-Lys-His-Cys-Phe-Glu-Ala-Gly (SEQ ID NO:451);

Gly-Ser-Ser-Arg-Leu-Cys-His-Met-Asp-Glu-Leu-Thr-His-Val-Cys-Val-His-Phe-Ala-Pro (SEQ ID NO:452);

Gly-Asp-Gly-Gly-Asn-Cys-Tyr-Thr-Asp-Ser-Leu-Thr-Lys-Leu-His-Phe-Cys-Met-Gly-Asp-Glu (SEQ ID NO:453);

Gly-Tyr-Asp-Val-Leu-Thr-Lys-Leu-Tyr-Phe-Val-Pro-Gly-Gly (SEQ ID NO:454);

Trp-Thr-Asp-Ser-Leu-Thr-Gly-Leu-Trp-Phe-Pro-Asp-Gly-Gly (SEQ ID NO:455);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:186);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:456);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:457);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Val (SEQ ID NO:189);

Ala-Asn-Trp-Phe-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:309);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Ser-Leu-Pro-Asp (SEQ ID NO:458);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Phe-Pro-Asp (SEQ ID NO:353);

Ala-Asn-Trp-Tyr-Asp-Ser-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:327).

9. A BLyS binding polypeptide comprising an amino acid sequence according to one of the following formulae:

(H) Cys-X<sub>2</sub>-Phe-X<sub>4</sub>-Trp-Glu-Cys (SEQ ID NO:8),

wherein

X<sub>2</sub> is Phe, Trp, or Tyr; and

X<sub>4</sub> is Pro or Tyr; or

(I) Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Cys (SEQ ID NO:9),

wherein

X<sub>2</sub> is Asp, Ile, Leu, or Tyr;

X<sub>3</sub> is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X<sub>4</sub> is His, Leu, Lys, or Phe;

X<sub>5</sub> is Leu, Pro, or Thr;

X<sub>6</sub> is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp; and

X<sub>7</sub> is Ala, Asn, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val; or

(J) Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (SEQ ID NO:10),

wherein

X<sub>2</sub> is Asn, Asp, Pro, Ser, or Thr;

X<sub>3</sub> is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X<sub>4</sub> is Ala, Ile, Leu, Pro, Thr, or Val;

X<sub>5</sub> is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X<sub>6</sub> is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X<sub>7</sub> is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X<sub>8</sub> is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr; or

(K) Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-Cys (SEQ ID NO:11),

wherein

X<sub>2</sub> is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X<sub>3</sub> is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X<sub>4</sub> is Asp, His, Leu, or Ser;

X<sub>5</sub> is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X<sub>6</sub> is Ala, Arg, Asn, or Leu;

X<sub>7</sub> is Ile, Leu, Met, Pro, Ser, or Thr;

X<sub>8</sub> is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X<sub>9</sub> is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val; or

(L) Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (SEQ ID NO:12),

wherein

X<sub>2</sub> is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X<sub>3</sub> is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X<sub>4</sub> is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X<sub>5</sub> is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X<sub>6</sub> is Asp, Leu, Pro, Thr, or Val;

X<sub>7</sub> is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;

X<sub>8</sub> is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X<sub>9</sub> is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X<sub>10</sub> is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr; and

X<sub>11</sub> is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

10. The polypeptide according to Claim 9, wherein

(a) said polypeptide comprises an amino acid sequence of the formula:

Cys-X<sub>2</sub>-Phe-X<sub>4</sub>-Trp-Glu-Cys (SEQ ID NO:8), and the following amino acid positions are independently selected as follows: X<sub>2</sub> is Tyr; X<sub>4</sub> is Pro; or combinations of such selections; or

(b) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-Cys (SEQ ID NO:9), and the following amino acid positions are independently selected as follows: X<sub>2</sub> is Asp or Leu; X<sub>3</sub> is Glu or Leu; X<sub>4</sub> is His or Leu; X<sub>5</sub> is Thr or Pro; X<sub>6</sub> is Lys; or combinations of such selections; or

(c) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-Cys (SEQ ID NO:10),

and the following amino acid positions are independently selected as follows: X<sub>2</sub> is Asp; X<sub>3</sub> is Ile; X<sub>4</sub> is Val or Leu; X<sub>5</sub> is Thr; X<sub>6</sub> is Leu; X<sub>8</sub> is Ser; or combinations of such selections; or

(d) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-Cys (SEQ ID NO:11), and the following amino acid positions are independently selected as follows: X<sub>4</sub> is Asp; X<sub>5</sub> is Glu or Pro; X<sub>6</sub> is Leu; X<sub>7</sub> is Thr; or combinations of such selections; or

(e) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys (SEQ ID NO:12),

and the following amino acid positions are independently selected as follows: X<sub>2</sub> is Trp, Tyr, or Val; X<sub>3</sub> is Asp; X<sub>4</sub> is Asp; X<sub>5</sub> is Leu; X<sub>6</sub> is Leu or Thr; X<sub>7</sub> is Lys or Thr; X<sub>8</sub> is Arg or Leu; X<sub>9</sub> is Thr or Trp; X<sub>10</sub> is Met or Phe; X<sub>11</sub> is Val; or combinations of such selections.

11. A BLYS binding polypeptide comprising an amino acid sequence of the following formula:

(A) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-Phe-X<sub>7</sub>-Trp-Glu-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:1),

wherein

X<sub>1</sub> is Ala, Asn, Lys, or Ser;

X<sub>2</sub> is Ala, Glu, Met, Ser, or Val;

X<sub>3</sub> is Ala, Asn, Lys, or Pro;

X<sub>5</sub> is Phe, Trp, or Tyr;

X<sub>7</sub> is Pro or Tyr;

X<sub>11</sub> is Ala, Gln, His, Phe, or Val;

X<sub>12</sub> is Asn, Gln, Gly, His, Ser, or Val; and

X<sub>13</sub> is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:2),

wherein

X<sub>1</sub> is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X<sub>2</sub> is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X<sub>5</sub> is Asp, Ile, Leu, or Tyr;

X<sub>6</sub> is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X<sub>7</sub> is His, Leu, Lys, or Phe;

X<sub>8</sub> is Leu, Pro, or Thr;

X<sub>9</sub> is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X<sub>10</sub> is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X<sub>12</sub> is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X<sub>13</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X<sub>14</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (SEQ ID NO:3),

wherein

X<sub>1</sub> is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X<sub>2</sub> is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X<sub>3</sub> is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X<sub>5</sub> is Asn, Asp, Pro, Ser, or Thr;

X<sub>6</sub> is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X<sub>7</sub> is Ala, Ile, Leu, Pro, Thr, or Val;

X<sub>8</sub> is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X<sub>9</sub> is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X<sub>10</sub> is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X<sub>11</sub> is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X<sub>13</sub> is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X<sub>14</sub> is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X<sub>15</sub> is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys-X<sub>14</sub>-X<sub>15</sub>-X<sub>16</sub> (SEQ ID NO:4),

wherein

X<sub>1</sub> is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X<sub>2</sub> is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X<sub>3</sub> is Asn, Asp, Leu, Pro, Ser, or Val;

X<sub>5</sub> is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X<sub>6</sub> is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X<sub>7</sub> is Asp, His, Leu, or Ser;

X<sub>8</sub> is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X<sub>9</sub> is Ala, Arg, Asn, or Leu;

X<sub>10</sub> is Ile, Leu, Met, Pro, Ser, or Thr;

X<sub>11</sub> is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X<sub>12</sub> is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X<sub>14</sub> is Asp, Gly, Leu, Phe, Tyr, or Val;

X<sub>15</sub> is Asn, His, Leu, Pro, or Tyr; and

X<sub>16</sub> is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub>

(SEQ ID NO:5),

wherein

X<sub>1</sub> is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X<sub>3</sub> is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;

X<sub>5</sub> is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X<sub>6</sub> is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X<sub>7</sub> is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X<sub>8</sub> is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X<sub>9</sub> is Asp, Leu, Pro, Thr, or Val;

X<sub>10</sub> is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;

X<sub>11</sub> is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X<sub>12</sub> is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X<sub>13</sub> is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;

X<sub>14</sub> is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;

X<sub>16</sub> is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;

X<sub>17</sub> is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X<sub>18</sub> is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub> (SEQ ID NO:6),

wherein

X<sub>1</sub> is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;

X<sub>2</sub> is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;

X<sub>3</sub> is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;

X<sub>4</sub> is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;

X<sub>5</sub> is Asp, Leu, Lys, Phe, Pro, Ser, or Val;

X<sub>6</sub> is His, Ile, Leu, Pro, Ser, or Thr;

X<sub>7</sub> is Arg, Gly, His, Leu, Lys, Met, or Thr;

X<sub>8</sub> is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;

X<sub>9</sub> is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;

X<sub>10</sub> is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;

X<sub>11</sub> is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and

X<sub>12</sub> is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:7),

wherein

X<sub>1</sub> is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;

X<sub>2</sub> is Arg, Gln, His, Ile, Leu, or Pro;

X<sub>3</sub> is Asp, Gly, Ile, Lys, Thr, Tyr or Val;

X<sub>4</sub> is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;

X<sub>5</sub> is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;

X<sub>6</sub> is Asp, Glu, His, Leu, Lys, Pro, or Val;

X<sub>7</sub> is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;

X<sub>8</sub> is Gln, Gly, His, Leu, Met, Ser, or Thr;

X<sub>9</sub> is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;

X<sub>10</sub> is Ala, Gly, Ile, Leu, Lys, Met, or Phe;

X<sub>11</sub> is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;

X<sub>12</sub> is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and

X<sub>13</sub> is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.



12. The BLYS binding polypeptide according to Claim 11, wherein

(a) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-Phe-X_7-Trp-Glu-Cys-X_{11}-X_{12}-X_{13}$  (SEQ ID NO:1), and the following amino acid positions are independently selected as follows:  $X_3$  is Lys;  $X_5$  is Tyr;  $X_7$  is Pro;  $X_{11}$  is Ala, Gln, His, Phe, or Val;  $X_{12}$  is Asn, Gln, Gly, His, Ser, or Val;  $X_{13}$  is Ala, Asn, Gly, Ile, Pro, or Ser; or combinations of such selections; or

(b) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14}$  (SEQ ID NO:2), and the following amino acid positions are independently selected as follows:  $X_3$  is Asp;  $X_5$  is Asp or Leu;  $X_6$  is Glu or Leu;  $X_7$  is His or Leu;  $X_8$  is Thr or Pro;  $X_9$  is Lys; or combinations of such selections; or

(c) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15}$  (SEQ ID NO:3), and the following amino acid positions are independently selected as follows:  $X_3$  is Ala;  $X_5$  is Asp;  $X_6$  is Ile;  $X_7$  is Val or Leu;  $X_8$  is Thr;  $X_9$  is Leu;  $X_{11}$  is Ser;  $X_{13}$  is Val;  $X_{15}$  is Glu or Pro; or combinations of such selections; or

(d) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-Cys-X_{14}-X_{15}-X_{16}$  (SEQ ID NO:4), and the following amino acid positions are independently selected as follows:  $X_1$  is Ser;  $X_2$  is Arg;  $X_3$  is Asn or Asp;  $X_7$  is Asp;  $X_8$  is Glu or Pro;  $X_9$  is Leu;  $X_{10}$  is Thr;  $X_{14}$  is Leu;  $X_{15}$  is His, Leu, or Pro;  $X_{16}$  is Asp or Ser; or combinations of such selections; or

(e) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18}$  (SEQ ID NO:5), and the following amino acid positions are independently selected as follows:  $X_1$  is Arg;  $X_2$  is Asn, Asp, Gly, or Pro;  $X_3$  is Gly or Met;  $X_5$  is Trp, Tyr, or Val;  $X_6$  is Asp;  $X_7$  is Asp;  $X_8$  is Leu;  $X_9$  is Leu or Thr;  $X_{10}$  is Lys or Thr;  $X_{11}$  is Arg or Leu;  $X_{12}$  is Thr or Trp;  $X_{13}$  is Met or Phe;  $X_{14}$  is Val;  $X_{16}$  is Met;  $X_{17}$  is Arg, His, or Tyr;  $X_{18}$  is Asn or His; or combinations of such selections; or

(f) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}$  (SEQ ID NO:6), and the following amino acid positions are independently selected as follows:  $X_1$  is Gly, Tyr, or Val;  $X_2$  is

His or Tyr; X<sub>3</sub> is Asp or Tyr; X<sub>4</sub> is Asp or Gln; X<sub>5</sub> is Leu or Ser; X<sub>6</sub> is Leu or Thr; X<sub>7</sub> is Lys or Thr; X<sub>8</sub> is Leu or Lys; X<sub>9</sub> is Met or Ser; X<sub>10</sub> is Thr or Leu; X<sub>11</sub> is Pro or Thr; X<sub>12</sub> is Arg or Pro; or combinations of such selections; or

(g) said polypeptide includes an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:7), and the following amino acid positions are independently selected as follows: X<sub>1</sub> is Glu or Lys; X<sub>2</sub> is His or Pro; X<sub>3</sub> is Tyr; X<sub>4</sub> is Asp or Gln; X<sub>5</sub> is Asn or Thr; X<sub>6</sub> is Asp or Pro; X<sub>7</sub> is Ile or Pro; X<sub>8</sub> is Leu or Thr; X<sub>9</sub> is Lys; X<sub>10</sub> is Gly or Met; X<sub>11</sub> is Ala or Thr; X<sub>12</sub> is Arg or His; X<sub>13</sub> is His; or combinations of such selections.

13. The BLyS binding polypeptide according to Claim 11, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-162 as depicted in Tables 1-8.

14. The BLyS binding polypeptide according to Claim 11, comprising an amino acid sequence selected from the group consisting of:

AGKEPCYFYWECAVSGPGPEGGGK (SEQ ID NO:163),  
AGVPFCDLLTKHCFEAGPGPEGGGK (SEQ ID NO:164),  
GSSRLCHMDELTHVCVHFAPPGPEGGGK (SEQ ID NO:165),  
GDGGNCYTDSLTKLHFCMGDEPGPEGGGK (SEQ ID NO:166),  
GYDVLTKLYFVPPGGPGPEGGGK (SEQ ID NO:167), and  
WTDSLTLGLWFPDGGPGPEGGGK, (SEQ ID NO:168).

15. A recombinant bacteriophage expressing exogenous DNA encoding a BLyS binding polypeptide comprising an amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

16. The bacteriophage according to Claim 15, wherein Xaa is Pro or Ser.

17. The bacteriophage according to Claim 15, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

Ala-Gly-Lys-Glu-Pro-Cys-Tyr-Phe-Tyr-Trp-Glu-Cys-Ala-Val-Ser-Gly (SEQ ID NO:450);

Ala-Gly-Val-Pro-Phe-Cys-Asp-Leu-Leu-Thr-Lys-His-Cys-Phe-Glu-Ala-Gly (SEQ ID NO:451);

Gly-Ser-Ser-Arg-Leu-Cys-His-Met-Asp-Glu-Leu-Thr-His-Val-Cys-Val-His-Phe-Ala-Pro (SEQ ID NO:452);

Gly-Asp-Gly-Gly-Asn-Cys-Tyr-Thr-Asp-Ser-Leu-Thr-Lys-Leu-His-Phe-Cys-Met-Gly-Asp-Glu (SEQ ID NO:453);

Gly-Tyr-Asp-Val-Leu-Thr-Lys-Leu-Tyr-Phe-Val-Pro-Gly-Gly (SEQ ID NO:454);

Trp-Thr-Asp-Ser-Leu-Thr-Gly-Leu-Trp-Phe-Pro-Asp-Gly-Gly (SEQ ID NO:455);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:186);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:456);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:457);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Val (SEQ ID NO:189);

Ala-Asn-Trp-Phe-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:309);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Ser-Leu-Pro-Asp (SEQ ID NO:458);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Phe-Pro-Asp (SEQ ID NO:353);

Ala-Asn-Trp-Tyr-Asp-Ser-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:327).

18. The bacteriophage according to Claim 15, wherein said polypeptides comprises the amino acid sequence:  $X_1-X_2-Asp-X_4-Leu-Thr-X_7-Leu-X_9-X_{10}$  (SEQ ID NO:448), wherein

$X_1$  is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

$X_2$  is Tyr, Phe, Glu, Cys, Asn;

$X_4$  is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

$X_7$  is Lys, Asn, Gln, Gly, or Arg;

$X_9$  is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

$X_{10}$  is Leu, Phe, Val, Ile, or His.

19. The bacteriophage according to Claim 18, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

20. The bacteriophage according to Claim 18, wherein said polypeptide comprises the amino acid sequence: Ala-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Asp-X<sub>6</sub>-Leu-Thr-X<sub>9</sub>-Leu-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:447),

wherein

X<sub>2</sub> is any amino acid except Arg;

X<sub>3</sub> is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X<sub>4</sub> is Tyr, Phe, Glu, Cys, Asn;

X<sub>6</sub> is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X<sub>9</sub> is Lys, Asn, Gln, Gly, or Arg;

X<sub>11</sub> is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X<sub>12</sub> is Leu, Phe, Val, Ile, or His;

X<sub>13</sub> is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X<sub>14</sub> is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

21. The bacteriophage according to Claim 18, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

22. A recombinant bacteriophage expressing exogenous DNA encoding a BLyS binding polypeptide comprising an amino acid sequence of the formula:

(A) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-Phe-X<sub>7</sub>-Trp-Glu-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:1),

wherein

X<sub>1</sub> is Ala, Asn, Lys, or Ser;

X<sub>2</sub> is Ala, Glu, Met, Ser, or Val;

X<sub>3</sub> is Ala, Asn, Lys, or Pro;

X<sub>5</sub> is Phe, Trp, or Tyr;

X<sub>7</sub> is Pro or Tyr;

X<sub>11</sub> is Ala, Gln, His, Phe, or Val;

X<sub>12</sub> is Asn, Gln, Gly, His, Ser, or Val; and

X<sub>13</sub> is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:2),

wherein

X<sub>1</sub> is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X<sub>2</sub> is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X<sub>5</sub> is Asp, Ile, Leu, or Tyr;

X<sub>6</sub> is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X<sub>7</sub> is His, Leu, Lys, or Phe;

X<sub>8</sub> is Leu, Pro, or Thr;

X<sub>9</sub> is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X<sub>10</sub> is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X<sub>12</sub> is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X<sub>13</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X<sub>14</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (SEQ ID NO:3),

wherein

X<sub>1</sub> is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X<sub>2</sub> is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X<sub>3</sub> is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X<sub>5</sub> is Asn, Asp, Pro, Ser, or Thr;

X<sub>6</sub> is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X<sub>7</sub> is Ala, Ile, Leu, Pro, Thr, or Val;

X<sub>8</sub> is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X<sub>9</sub> is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X<sub>10</sub> is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X<sub>11</sub> is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X<sub>13</sub> is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X<sub>14</sub> is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X<sub>15</sub> is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys-X<sub>14</sub>-X<sub>15</sub>-X<sub>16</sub>

(SEQ ID NO:4),

wherein

X<sub>1</sub> is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X<sub>2</sub> is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X<sub>3</sub> is Asn, Asp, Leu, Pro, Ser, or Val;

X<sub>5</sub> is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X<sub>6</sub> is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X<sub>7</sub> is Asp, His, Leu, or Ser;

X<sub>8</sub> is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X<sub>9</sub> is Ala, Arg, Asn, or Leu;

X<sub>10</sub> is Ile, Leu, Met, Pro, Ser, or Thr;

X<sub>11</sub> is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X<sub>12</sub> is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X<sub>14</sub> is Asp, Gly, Leu, Phe, Tyr, or Val;

X<sub>15</sub> is Asn, His, Leu, Pro, or Tyr; and

X<sub>16</sub> is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub>

(SEQ ID NO:5),

wherein

X<sub>1</sub> is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X<sub>3</sub> is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;

X<sub>5</sub> is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X<sub>6</sub> is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X<sub>7</sub> is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

$X_8$  is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;  
 $X_9$  is Asp, Leu, Pro, Thr, or Val;  
 $X_{10}$  is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;  
 $X_{11}$  is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;  
 $X_{12}$  is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;  
 $X_{13}$  is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;  
 $X_{14}$  is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;  
 $X_{16}$  is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;  
 $X_{17}$  is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and  
 $X_{18}$  is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F)  $X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}$  (SEQ ID NO:6),

wherein

$X_1$  is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;  
 $X_2$  is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;  
 $X_3$  is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;  
 $X_4$  is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;  
 $X_5$  is Asp, Leu, Lys, Phe, Pro, Ser, or Val;  
 $X_6$  is His, Ile, Leu, Pro, Ser, or Thr;  
 $X_7$  is Arg, Gly, His, Leu, Lys, Met, or Thr;  
 $X_8$  is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;  
 $X_9$  is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;  
 $X_{10}$  is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;  
 $X_{11}$  is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and  
 $X_{12}$  is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G)  $X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}$  (SEQ ID NO:7),

wherein

$X_1$  is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;  
 $X_2$  is Arg, Gln, His, Ile, Leu, or Pro;  
 $X_3$  is Asp, Gly, Ile, Lys, Thr, Tyr or Val;  
 $X_4$  is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;  
 $X_5$  is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;

X<sub>6</sub> is Asp, Glu, His, Leu, Lys, Pro, or Val;  
X<sub>7</sub> is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;  
X<sub>8</sub> is Gln, Gly, His, Leu, Met, Ser, or Thr;  
X<sub>9</sub> is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;  
X<sub>10</sub> is Ala, Gly, Ile, Leu, Lys, Met, or Phe;  
X<sub>11</sub> is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;  
X<sub>12</sub> is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and  
X<sub>13</sub> is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

23. The recombinant bacteriophage according to Claim 22, wherein

(a) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-Phe-X<sub>7</sub>-Trp-Glu-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:1), and the following amino acid positions are independently selected as follows: X<sub>3</sub> is Lys; X<sub>5</sub> is Tyr; X<sub>7</sub> is Pro; X<sub>11</sub> is Ala, Gln, His, Phe, or Val; X<sub>12</sub> is Asn, Gln, Gly, His, Ser, or Val; X<sub>13</sub> is Ala, Asn, Gly, Ile, Pro, or Ser; or combinations of such selections; or

(b) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:2), and the following amino acid positions are independently selected as follows: X<sub>3</sub> is Asp; X<sub>5</sub> is Asp or Leu; X<sub>6</sub> is Glu or Leu; X<sub>7</sub> is His or Leu; X<sub>8</sub> is Thr or Pro; X<sub>9</sub> is Lys; or combinations of such selections; or

(c) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (SEQ ID NO:3), and the following amino acid positions are independently selected as follows: X<sub>3</sub> is Ala; X<sub>5</sub> is Asp; X<sub>6</sub> is Ile; X<sub>7</sub> is Val or Leu; X<sub>8</sub> is Thr; X<sub>9</sub> is Leu; X<sub>11</sub> is Ser; X<sub>13</sub> is Val; X<sub>15</sub> is Glu or Pro; or combinations of such selections; or

(d) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys-X<sub>14</sub>-X<sub>15</sub>-X<sub>16</sub> (SEQ ID NO:4), and the following amino acid positions are independently selected as follows: X<sub>1</sub> is Ser; X<sub>2</sub> is Arg; X<sub>3</sub> is Asn or Asp; X<sub>7</sub> is Asp; X<sub>8</sub> is Glu or Pro; X<sub>9</sub> is Leu; X<sub>10</sub> is Thr; X<sub>14</sub> is Leu; X<sub>15</sub> is His, Leu, or Pro; X<sub>16</sub> is Asp or Ser; or combinations of such selections; or

(e) said polypeptide comprises an amino acid sequence of the following formula:



X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub> (SEQ ID NO:5), and the following amino acid positions are independently selected as follows: X<sub>1</sub> is Arg; X<sub>2</sub> is Asn, Asp, Gly, or Pro; X<sub>3</sub> is Gly or Met; X<sub>5</sub> is Trp, Tyr, or Val; X<sub>6</sub> is Asp; X<sub>7</sub> is Asp; X<sub>8</sub> is Leu; X<sub>9</sub> is Leu or Thr; X<sub>10</sub> is Lys or Thr; X<sub>11</sub> is Arg or Leu; X<sub>12</sub> is Thr or Trp; X<sub>13</sub> is Met or Phe; X<sub>14</sub> is Val; X<sub>16</sub> is Met; X<sub>17</sub> is Arg, His, or Tyr; X<sub>18</sub> is Asn or His; or combinations of such selections; or

(f) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub> (SEQ ID NO:6), and the following amino acid positions are independently selected as follows: X<sub>1</sub> is Gly, Tyr, or Val; X<sub>2</sub> is His or Tyr; X<sub>3</sub> is Asp or Tyr; X<sub>4</sub> is Asp or Gln; X<sub>5</sub> is Leu or Ser; X<sub>6</sub> is Leu or Thr; X<sub>7</sub> is Lys or Thr; X<sub>8</sub> is Leu or Lys; X<sub>9</sub> is Met or Ser; X<sub>10</sub> is Thr or Leu; X<sub>11</sub> is Pro or Thr; X<sub>12</sub> is Arg or Pro; or combinations of such selections; or

(g) said polypeptide comprises an amino acid sequence of the following formula:

X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:7), and the following amino acid positions are independently selected as follows: X<sub>1</sub> is Glu or Lys; X<sub>2</sub> is His or Pro; X<sub>3</sub> is Tyr; X<sub>4</sub> is Asp or Gln; X<sub>5</sub> is Asn or Thr; X<sub>6</sub> is Asp or Pro; X<sub>7</sub> is Ile or Pro; X<sub>8</sub> is Leu or Thr; X<sub>9</sub> is Lys; X<sub>10</sub> is Gly or Met; X<sub>11</sub> is Ala or Thr; X<sub>12</sub> is Arg or His; X<sub>13</sub> is His; or combinations of such selections.

24. A method for detecting BLYS or a BLYS-like polypeptide in a solution suspected of containing it comprising:

- (a) contacting said solution with a polypeptide according to any of Claims 1, 9 or 11, and
- (b) determining whether binding has occurred between said polypeptide and BLYS or a BLYS-like polypeptide.

25. A method for purifying BLYS or a BLYS-like polypeptide comprising:

- (a) immobilizing a binding polypeptide according to any of Claims 1, 9 or 11 on a solid support;
- (b) contacting a solution containing BLYS or a BLYS-like polypeptide with said support; and, thereafter,
- (c) separating the solution from said support.

26. BLYS separation media comprising:
- (a) a chromatographic matrix material, and, immobilized thereon,
  - (b) a BLYS binding molecule comprising a BLYS binding polypeptide as defined in any of Claims 1, 9 or 11.
27. The BLYS separation media according to Claim 26, comprising:
- (a) a chromatographic matrix material, and, immobilized thereon,
  - (b) a BLYS binding molecule comprising a BLYS binding polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:20-162 and 186-435, as depicted in Tables 1-8 and 14.
28. A method for separating BLYS or a BLYS-like polypeptide from a solution containing it comprising:
- (a) contacting said solution with separation media as defined in Claim 26,
  - (b) removing unbound material, and
  - (c) eluting bound BLYS or BLYS-like polypeptide from said separation media.
29. A polynucleotide encoding a BLYS binding polypeptide comprising the amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.
30. The polynucleotide according to Claim 29, wherein Xaa is Pro or Ser.
31. The polynucleotide according to Claim 29, wherein said polypeptides comprises the amino acid sequence:  $X_1$ - $X_2$ -Asp- $X_4$ -Leu-Thr- $X_7$ -Leu- $X_9$ - $X_{10}$  (SEQ ID NO:448), wherein
- $X_1$  is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;
  - $X_2$  is Tyr, Phe, Glu, Cys, Asn;
  - $X_4$  is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;
  - $X_7$  is Lys, Asn, Gln, Gly, or Arg;

X<sub>9</sub> is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

X<sub>10</sub> is Leu, Phe, Val, Ile, or His.

32. The polynucleotide according to Claim 31, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

33. The polynucleotide according to Claim 31, wherein said polypeptide comprises the amino acid sequence: Ala-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Asp-X<sub>6</sub>-Leu-Thr-X<sub>9</sub>-Leu-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:447),

wherein

X<sub>2</sub> is any amino acid except Arg;

X<sub>3</sub> is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X<sub>4</sub> is Tyr, Phe, Glu, Cys, Asn;

X<sub>6</sub> is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X<sub>9</sub> is Lys, Asn, Gln, Gly, or Arg;

X<sub>11</sub> is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X<sub>12</sub> is Leu, Phe, Val, Ile, or His;

X<sub>13</sub> is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X<sub>14</sub> is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

34. The polynucleotide according to Claim 31, encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

35. A polynucleotide encoding a BLYS binding polypeptide of the formula:

(A) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-Phe-X<sub>7</sub>-Trp-Glu-Cys-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub> (SEQ ID NO:1),

wherein

X<sub>1</sub> is Ala, Asn, Lys, or Ser;

X<sub>2</sub> is Ala, Glu, Met, Ser, or Val;

X<sub>3</sub> is Ala, Asn, Lys, or Pro;

X<sub>5</sub> is Phe, Trp, or Tyr;

X<sub>7</sub> is Pro or Tyr;

X<sub>11</sub> is Ala, Gln, His, Phe, or Val;

X<sub>12</sub> is Asn, Gln, Gly, His, Ser, or Val; and

X<sub>13</sub> is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-Cys-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:2),

wherein

X<sub>1</sub> is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X<sub>2</sub> is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X<sub>3</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X<sub>5</sub> is Asp, Ile, Leu, or Tyr;

X<sub>6</sub> is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X<sub>7</sub> is His, Leu, Lys, or Phe;

X<sub>8</sub> is Leu, Pro, or Thr;

X<sub>9</sub> is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X<sub>10</sub> is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X<sub>12</sub> is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X<sub>13</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X<sub>14</sub> is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-Cys-X<sub>13</sub>-X<sub>14</sub>-X<sub>15</sub> (SEQ ID NO:3),

wherein

X<sub>1</sub> is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X<sub>2</sub> is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X<sub>3</sub> is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X<sub>5</sub> is Asn, Asp, Pro, Ser, or Thr;

X<sub>6</sub> is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X<sub>7</sub> is Ala, Ile, Leu, Pro, Thr, or Val;

X<sub>8</sub> is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X<sub>9</sub> is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X<sub>10</sub> is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X<sub>11</sub> is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X<sub>13</sub> is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X<sub>14</sub> is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X<sub>15</sub> is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-Cys-X<sub>14</sub>-X<sub>15</sub>-X<sub>16</sub> (SEQ ID NO:4),

wherein

X<sub>1</sub> is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X<sub>2</sub> is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X<sub>3</sub> is Asn, Asp, Leu, Pro, Ser, or Val;

X<sub>5</sub> is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X<sub>6</sub> is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X<sub>7</sub> is Asp, His, Leu, or Ser;

X<sub>8</sub> is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X<sub>9</sub> is Ala, Arg, Asn, or Leu;

X<sub>10</sub> is Ile, Leu, Met, Pro, Ser, or Thr;

X<sub>11</sub> is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X<sub>12</sub> is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X<sub>14</sub> is Asp, Gly, Leu, Phe, Tyr, or Val;

X<sub>15</sub> is Asn, His, Leu, Pro, or Tyr; and

X<sub>16</sub> is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X<sub>1</sub>-X<sub>2</sub>-X<sub>3</sub>-Cys-X<sub>5</sub>-X<sub>6</sub>-X<sub>7</sub>-X<sub>8</sub>-X<sub>9</sub>-X<sub>10</sub>-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub>-Cys-X<sub>16</sub>-X<sub>17</sub>-X<sub>18</sub>  
(SEQ ID NO:5),

wherein

X<sub>1</sub> is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X<sub>2</sub> is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X<sub>3</sub> is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;



X<sub>3</sub> is Asp, Gly, Ile, Lys, Thr, Tyr or Val;  
 X<sub>4</sub> is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;  
 X<sub>5</sub> is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;  
 X<sub>6</sub> is Asp, Glu, His, Leu, Lys, Pro, or Val;  
 X<sub>7</sub> is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;  
 X<sub>8</sub> is Gln, Gly, His, Leu, Met, Ser, or Thr;  
 X<sub>9</sub> is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;  
 X<sub>10</sub> is Ala, Gly, Ile, Leu, Lys, Met, or Phe;  
 X<sub>11</sub> is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;  
 X<sub>12</sub> is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and  
 X<sub>13</sub> is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

36. A method for identifying a binding molecule for a BLyS target comprising the steps of utilizing a BLyS binding polypeptide according to any of Claims 1, 9 or 11 to form a complex with BLyS or a BLyS-like polypeptide, contacting said complex with one or more potential BLyS target binding molecules, and determining whether said one or more potential BLyS target binding molecules competes with said BLyS binding polypeptide to form a complex with said BLyS or BLyS-like polypeptide.

37. A BLyS affinity maturation library, comprising a population of at least 10<sup>3</sup> polypeptides, wherein the polypeptides of said population comprise the amino acid sequence:

Ala-X<sub>2</sub>-X<sub>3</sub>-X<sub>4</sub>-Asp-X<sub>6</sub>-Leu-Thr-X<sub>9</sub>-Leu-X<sub>11</sub>-X<sub>12</sub>-X<sub>13</sub>-X<sub>14</sub> (SEQ ID NO:449),  
 wherein

X<sub>2</sub> is any amino acid;  
 X<sub>3</sub> is any amino acid;  
 X<sub>4</sub> is any amino acid;  
 X<sub>6</sub> is any amino acid;  
 X<sub>9</sub> is any amino acid;  
 X<sub>11</sub> is any amino acid;

X<sub>12</sub> is any amino acid;  
X<sub>13</sub> is any amino acid; and  
X<sub>14</sub> is any amino acid.

38. A DNA template encoding a multiplicity of BLyS binding polypeptides, comprising the sequence:

GCT NNN NNN NNN GAT NNN CTT ACT NNN CTC NNN NNN NNN NNN (SEQ ID NO:185).